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1: Okuda D, Horii K, Mizuno H, Morita T. Related Articles, Links

Characterization and preliminary crystallographic studies of EMS16, an antagonist of collagen receptor (GPIa/IIa) from the venom of Echis multisquamatus.
J Biochem (Tokyo). 2003 Jul;134(1):19-23.
PMID: 12944366 [PubMed - indexed for MEDLINE]

2: Augustin A, Muller-Steffner H, Schuber F. Related Articles, Links

Molecular cloning and functional expression of bovine spleen ecto-NAD+ glycohydrolase: structural identity with human CD38.
Biochem J. 2000 Jan 1;345 Pt 1:43-52.
PMID: 10600637 [PubMed - indexed for MEDLINE]

3: Bourrat C, Radisson J, Chavassieux P, Azzar G, Roux B, Meunier PJ. Related Articles, Links

Activity increase after extraction of alkaline phosphatase from human osteoblastic membranes by nonionic detergents: influence of age and sex.
Calcif Tissue Int. 2000 Jan;66(1):22-8.
PMID: 10602840 [PubMed - indexed for MEDLINE]

4: Del Vecchio Blanco F, Bolognesi A, Malorni A, Sande MJ, Savino G, Parente A. Related Articles, Links

Complete amino-acid sequence of PD-S2, a new ribosome-inactivating protein from seeds of Phytolacca dioica L.
Biochim Biophys Acta. 1997 Mar 7;1338(1):137-44.
PMID: 9074624 [PubMed - indexed for MEDLINE]

5: Munishkin A, Wool IG. Related Articles, Links

Systematic deletion analysis of ricin A-chain function. Single amino acid deletions.
J Biol Chem. 1995 Dec 22;270(51):30581-7.
PMID: 8530493 [PubMed - indexed for MEDLINE]

☐ **6:** Yoshino M, Takagi T. Related Articles, Links

Subunit structure of AMP nucleosidase from Azotobacter vinelandii.
J Biochem (Tokyo). 1973 Dec;74(6):1151-6. No abstract available.
PMID: 4781054 [PubMed - indexed for MEDLINE]

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Enzymatic polymerization behavior using cellulose-binding domain deficient endoglucanase II.
Macromol Biosci. 2005 Jul 14;5(7):623-8.
PMID: 15988789 [PubMed - indexed for MEDLINE]

2: Zhou W, Irwin DC, Escovar-Kousen J, Wilson DB. Related Articles, Links

Kinetic studies of Thermobifida fusca Cel9A active site mutant enzymes.
Biochemistry. 2004 Aug 3;43(30):9655-63.
PMID: 15274620 [PubMed - indexed for MEDLINE]

3: Mandelman D, Belaich A, Belaich JP, Aghajari N, Driguez H, Haser R. Related Articles, Links

X-Ray crystal structure of the multidomain endoglucanase Cel9G from Clostridium cellulolyticum complexed with natural and synthetic cello-oligosaccharides.
J Bacteriol. 2003 Jul;185(14):4127-35.
PMID: 12837787 [PubMed - indexed for MEDLINE]

4: Kataeva IA, Seidel RD 3rd, Shah A, West LT, Li XL, Ljungdahl LG. Related Articles, Links

The fibronectin type 3-like repeat from the Clostridium thermocellum cellobiohydrolase CbhA promotes hydrolysis of cellulose by modifying its surface.
Appl Environ Microbiol. 2002 Sep;68(9):4292-300.
PMID: 12200278 [PubMed - indexed for MEDLINE]

5: Saloheimo M, Paloheimo M, Hakola S, Pere J, Swanson B, Nyyssonen E, Bhatia A, Ward Related Articles, Links

M, Penttila M.

Swollenin, a Trichoderma reesei protein with sequence similarity to the plant expansins, exhibits disruption activity on cellulosic materials.
Eur J Biochem. 2002 Sep;269(17):4202-11.
PMID: 12199698 [PubMed - indexed for MEDLINE]

6: Ding SY, Bayer EA, Steiner D, Shoham Y, Lamed R. Related Articles, Links

A scaffoldin of the Bacteroides cellulosolvens cellulosome that contains 11 type II cohesins.
J Bacteriol. 2000 Sep;182(17):4915-25.
PMID: 10940036 [PubMed - indexed for MEDLINE]

7: Riedel K, Ritter J, Bauer S, Bronnenmeier K. Related Articles, Links

The modular cellulase CelZ of the thermophilic bacterium Clostridium stercorarium contains a thermostabilizing domain.
FEMS Microbiol Lett. 1998 Jul 15;164(2):261-7.
PMID: 9682475 [PubMed - indexed for MEDLINE]

8: Zverlov V, Mahr S, Riedel K, Bronnenmeier K. Related Articles, Links

Properties and gene structure of a bifunctional cellulolytic enzyme (CelA) from the extreme thermophile 'Anaerocellum thermophilum' with separate glycosyl hydrolase family 9 and 48 catalytic domains.
Microbiology. 1998 Feb;144 (Pt 2):457-65.
PMID: 9493383 [PubMed - indexed for MEDLINE]

9: Sakon J, Irwin D, Wilson DB, Karplus PA. Related Articles, Links

Structure and mechanism of endo/exocellulase E4 from Thermomonospora fusca.
Nat Struct Biol. 1997 Oct;4(10):810-8.
PMID: 9334746 [PubMed - indexed for MEDLINE]

10: Pages S, Gal L, Belaich A, Gaudin C, Tardif C, Belaich JP. Related Articles, Links

Role of scaffolding protein CipC of Clostridium cellulolyticum in cellulose degradation.
J Bacteriol. 1997 May;179(9):2810-6.
PMID: 9139893 [PubMed - indexed for MEDLINE]

11: Macarron R, Henrissat B, Claeyssens M. Related Articles, Links

Family A cellulases: two essential tryptophan residues in endoglucanase III from Trichoderma reesei.
Biochim Biophys Acta. 1995 Oct 19;1245(2):187-90.

PMID: 7492576 [PubMed - indexed for MEDLINE]

□ **12:** Lassig JP, Shultz MD, Gooch MG, Evans BR, Woodward J. Related Articles, Links

Inhibition of cellobiohydrolase I from Trichoderma reesei by palladium.
Arch Biochem Biophys. 1995 Sep 10;322(1):119-26.
PMID: 7574665 [PubMed - indexed for MEDLINE]

□ **13:** Goldstein MA, Doi RH. Related Articles, Links

Mutation analysis of the cellulose-binding domain of the Clostridium cellulovorans cellulose-binding protein A.
J Bacteriol. 1994 Dec;176(23):7328-34.
PMID: 7961505 [PubMed - indexed for MEDLINE]

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L1         8600 (CARBOHYDRATE BINDING DOMAIN) OR (CBD)

=> S L1 (6a) (structure)
L2          178 L1 (6A) (STRUCTURE)

=> s l1 (w) III
L3            0 L1 (W) III

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L4            9 L2 AND REVIEW

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L5 ANSWER 1 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2006:184858 CAPLUS
TI Three-dimensional structure of glucodextranase, a glycoside hydrolase family 15 enzyme
AU Mizuno, Masahiro; Tonozuka, Takashi; Ichikawa, Kazuhiro; Kamitori, Shigehiro; Nishikawa, Atsushi; Sakano, Yoshiyuki
CS Department of Applied Science, Tokyo University of Agriculture and Technology, 3-5-8, Saiwai-cho, Fuchu, Tokyo, 183-8509, Japan
SO Biologia (Bratislava, Slovakia) (2005), 60(Suppl. 16), 171-176
CODEN: BLOAAO; ISSN: 0006-3088
PB Slovak Academy of Sciences
DT Journal
LA English
AB A glucodextranase (GDase) from Arthrobacter globiformis I42 hydrolyzes α-1,6-glucosidic linkages of dextran from the non-reducing end to produce β-D-glucose. Here, we **review** the crystal structures of GDase of the unliganded form and the complex with acarbose.

The structure of GDase is composed of four domains, N, A, B, and C.
Domain A forms an (α/α)6-barrel structure and domain N consists of 17 antiparallel β-strands. Both domains are conserved in bacterial glucoamylases (GAs) and appear to be mainly concerned with catalytic activity. The structure of GDase complexed with acarbose revealed that the positions and orientations of the residues at subsites -1 and +1 are nearly identical for GDase and GA; however, the residues corresponding to subsite +2, which form the entrance of the substrate-binding pocket, and the position of the open space and constriction of GDase are different from those of GAs. On the other hand, domains B and C are not found in bacterial GAs. The primary structure of domain C is homologous with the surface layer homol. domain of pullulanases, and the three-dimensional **structure** of domain C resembles the **carbohydrate-binding domain** of some glycohydrolases. The hydrophobicity of domain B is higher than that of the other three domains. These findings suggest that domains B and C serve as cell wall anchors and contribute to the effective degradation of dextran at the cell surface.

RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 2 OF 8 CAPLUS
AN 2005:503905 CAPLUS
DN 143:92803
TI X-ray crystallographic study of glucodextranase from a gram-positive bacterium, Arthrobacter globiformis I42
AU Mizuno, Masahiro; Tonozuka, Takashi; Ichikawa, Kazuhiro; Kamitori, Shigehiro; Nishikawa, Atsushi; Sakano, Yoshiyuki
CS United. Grad. Sch. Agric. Sci., Tokyo Univ. Agric. Technol., Fuchu, 183-8509, Japan
SO Journal of Applied Glycoscience (2005), 52(2), 145-151
CODEN: JAGLFX; ISSN: 1344-7882
PB Japanese Society of Applied Glycoscience
DT Journal; General Review
LA English
AB A **review**. Glucodextranase (GDase) hydrolyzes α-1,6-glucosidic linkages of dextran from the non-reducing end to

produce β-D-glucose. GDase is classified under GH15, whose major
member is glucoamylase (GA) that hydrolyzes α-1,4-glucosidic
linkages of starch. We have cloned a GDase gene from the gram-pos.
bacterium Arthrobacter globiformis I42 and determined the crystal structure at
2.42-Å resolution The structure of GDase is composed of four domains N,
A, B and C. Domain N consists of 17 antiparallel β-strands and
domain A forms and (α/α)6 barrel structure, which is conserved
between GAs. Furthermore, the complex structure with acarbose was also
determined at 2.42-Å resolution The structure of GDase complexed with
acarbose revealed that the positions and orientations of the residues at
subsites -1 and +1 are nearly identical for GDase and GA; however, Glu380
and Trp582 located at subsite +2, which form the entrance of the catalytic
pocket, and the position of the open space and constriction of GDase are
different from those of GAs. On the other hand, domains B and C are not
found in GAs. The primary structure of domain C is homologous with the
surface layer homol. (SLH) of pullulanases from Gram-pos. bacteria, and
the three-dimensional **structure** of domain C resembles the
carbohydrate-binding domain of some
glycohydrolases. The hydrophobicity of domain B is higher than that of
the other three domains. These findings suggest that domains B and C
serve as cell wall anchors and contribute to the effective degradation of
dextran at the cell surface.

L5 ANSWER 3 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2003:830926 CAPLUS
DN 140:58465
TI Cellulose-binding domains: Tools for innovation in cellulosic fiber
production and modification
AU Quentin, Michael; van der Valk, Henry; van Dam, Jan; de Jong, Ed
CS Department of Fibre and Paper Technology, ATO BV, Wageningen, 6700 AA,
Neth.
SO ACS Symposium Series (2003), 855(Applications of Enzymes to
Lignocellulosics), 132-155
CODEN: ACSMC8; ISSN: 0097-6156

PB American Chemical Society
DT Journal; General Review
LA English
AB A **review**. Plant cell walls are composed of cellulose, nature's most abundant macromol., and therefore represent a renewable resource of special tech. importance. Cellulose degrading enzymes involved in plant cell wall loosening (expansins), or produced by plant pathogenic microorganisms (cellulases), share similarities favoring the degradation of this highly crystalline substrate. Most of the cellulases and cell wall loosening expansins share a multi-domain **structure**, which includes a cellulose-binding domain (**CBD**). CBDs possess the intrinsic ability to strongly and specifically bind to cellulose. CBDs may be applied to engineer hybrid enzymes able to bind to cellulose on one end, and to display enzymic or chemical reactivity on the other, providing innovative solns. to modify cellulosic surfaces or to immobilize biocatalysts on it. In transgenic plants, CBDs influence polysaccharide synthesis and their assembly in the cell wall. Therefore, CBDs represent biotechnol. tools to modify cellulosic fibers either during their growth or during post harvest processing.
RE.CNT 125 THERE ARE 125 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L5 ANSWER 4 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:779465 CAPLUS
DN 134:38967
TI Phage display of cellulose binding domains for biotechnological application
AU Benhar, Itai; Tamarkin, Aviva; Marash, Lea; Berdichevsky, Yevgeny; Yaron, Sima; Shoham, Yuval; Lamed, Raphael; Bayer, Edward A.
CS Department of Molecular Microbiology and Biotechnology, The George S. Wise Faculty of Life Sciences, Tel-Aviv University, Ramat Aviv, Israel
SO ACS Symposium Series (2000), 769(Glycosyl Hydrolases for Biomass Conversion), 168-189
CODEN: ACSMC8; ISSN: 0097-6156
PB American Chemical Society
DT Journal; General Review
LA English
AB A **review** with 65 refs. In recent years, cellulose-binding domains (CBDs) derived from the cellulolytic systems of cellulose-degrading microorganisms have become a focal point of attention

for a wide range of biotechnol. applications. The low cost and availability of cellulose matrixes have rendered CBDs attractive as affinity tags for the purification and immobilization of a plethora of proteins. Intensive studies of cellulose degradation pathways and the identification of components of the cellulose-degrading machinery have contributed significantly to our understanding of the **structure** and function of **CBDs**. The time is now ripe to utilize engineered CBDs to improve existing applications and to devise novel ones.
Here we describe our recent results of expts. where the Clostridium thermocellum scaffoldin CBD was genetically engineered for such purposes.
We describe the development of a novel phage display system where the C. thermocellum CBD is displayed as a fusion protein with single-chain antibodies. Our system is a filamentous (M13) phage display system that enables the efficient isolation and.

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L5 ANSWER 5 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
AN 2000:710413 CAPLUS
DN 134:38648
TI The structure and function of cellulose-binding domain of cellulase
AU Wang, Tianhong; Wang, Chunhui; Gao, Peiji
CS The State Key Laboratory of Microbial Technology, Shandong University, Jinan, 250100, Peop. Rep. China
SO Shengwu Gongcheng Jinzhan (2000), 20(2), 37-40
CODEN: SGJHA2; ISSN: 1003-3505
PB Zhongguo Kexueyuan Wenxian Qingbao Zhongxin
DT Journal; General Review
LA Chinese
AB A discussion and **review** with 20 refs. Most cellulases consist of catalytic domains and cellulose binding domains(CBDs), which can bind to cellulose and are conserved in some amino acid sequences. Cellulose binding domains improve the binding and facilitate the activity of catalytic domains on the insol. substrate, but not on soluble substrate. The results of investigations on structure and function, and subsequent

mutagenesis of the CBDs indicated that CBDs rely on several aromatic amino acids for binding to the cellulose surfaces. Some experiment results showed that CBDs of exoglucanases are able to disrupt the crystalline cellulose, facilitate the enzymic degradation of cellulose. The structural domain as CBDs has been successfully used in purification and immobilization of numerous examples of fusion proteins. The improved understanding of the **structure** and function of **CBDs** are significant to understanding of enzymic functionary mechanism, and the development of cellulase biotechnol.

L5 ANSWER 6 OF 8 CAPLUS
AN 1998:330997 CAPLUS
DN 129:105755
TI The structure and function of cellulose binding domains
AU Boraston, A.; Bray, M.; Brun, E.; Creagh, A. L.; Gilkes, N. R.; Guarna, M. M.; Jervis, E.; Johnson, P.; Kormos, J.; Mcintosh, L.; Mclean, B. W.; Sandercock, L. E.; Tomme, P.; Haynes, C. A.; Warren, R. A. J.; Kilburn, D. G.
CS Protein Engineering Network of Centres of Excellence, Biotechnology Laboratory, University of British Columbia, Vancouver, V6T 1Z3, Can.
SO Special Publication - Royal Society of Chemistry (1998), 219(Carbohydrates from Trichoderma Reesei and Other Microorganisms), 139-146
CODEN: SROCDO; ISSN: 0260-6291
PB Royal Society of Chemistry
DT Journal; General Review
LA English
AB A **review** with 15 refs. More than 180 putative cellulose-binding domains (CBDs) have been identified and grouped into 13 families based on amino acid sequences. They vary in length from 33 to 240 amino acids. The **structures** of **CBDs** from five different families are now available. They all are anti-parallel β strand polypeptides. The authors have studied the properties of Family II and Family IV CBDs of β-glycanases from the cellulolytic bacterium Cellulomonas fimi in detail.
RE.CNT 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD

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L5 ANSWER 7 OF 8 EMBASE DUPLICATE 1

AN 94168662 EMBASE
DN 1994168662
TI The Clostridium cellulovorans cellulosome.
AU Doi R.H.; Goldstein M.; Hashida S.; Park J.-S.; Takagi M.
CS Molecular/Cellular Biology Section, University of California,Davis, CA 95616, United States
SO Critical Reviews in Microbiology, (1994) Vol. 20, No. 2, pp. 87-93. .
ISSN: 1040-841X CODEN: CRVMAC
CY United States
DT Journal; General Review
FS 004 Microbiology
LA English
SL English
ED Entered STN: 29 Jun 1994
Last Updated on STN: 29 Jun 1994
AB The Clostridium cellulovorans cellulosome is comprised of a large, nonenzymatic scaffolding protein called the cellulose binding protein A (CbpA) and a number of endoglucanases/xylanases. The CbpA contains several functional domains, including a signal peptide, a cellulose binding domain (CBD), a hydrophilic domain (HLD) present four times, and a hydrophobic domain (HBD) present nine times. The functions of the domains were studied by the construction of minigenes containing the putative functional domains and by expression of the minigenes in Escherichia coli. The purified product of the CBD was able to bind to various crystalline forms of cellulose and chitin with a K(d) of 1 μM. The binding capacity for CBD was a function of the crystallinity of the cellulose sample. Furthermore, the binding of CBD to Avicel was not inhibited by cellobiose or carboxymethylcellulose, suggesting that the **CBD** binding target was a three-dimensional **structure** found only in crystalline forms of cellulose. The HBD was tested for its ability to bind endoglucanases by an interaction Western as well as a sandwich enzyme immunoassay technique. The HBD was able to bind both EngB and EngD,

indicating that the HBD contained an endoglucanase binding
domain (EBD).
Because there are nine EBD domains, it is possible that CbpA can
bind up
to nine endoglucanases. The role of the HLDs remains elusive.
The data
indicate that the cellulosome is a complex enzyme containing a
scaffolding
protein (CbpA) to which is attached a number of endoglucanase
molecules.
This arrangement allows the complex to bind and degrade
crystalline
cellulose, which resists degradation by the free forms of
cellulosomal
endoglucanases.

L5 ANSWER 8 OF 8 CAPLUS COPYRIGHT 2006 ACS on STN
AN 1994:263906 CAPLUS
DN 120:263906
TI Lectins. Structures and lectin-sugar interactions
AU Yamamoto, Kazuo
CS Fac. Pharm. Sci., Univ. Tokyo, Tokyo, 113, Japan
SO Maku (1994), 19(1), 40-7
CODEN: MAKUD9; ISSN: 0385-1036
DT Journal; General Review
LA Japanese
AB A **review**, with 42 refs. Topics include: classification of
lectins, variety of sugar chain **structures**, determination of
carbohydrate-binding domains of legume
lectins, chemical synthesis of a lactose-binding domain
(nonapeptide),
construction of a chimeric lectin replaced with another
nonapeptide from a
lectin having a different carbohydrate-binding specificity, and
conformation of the carbohydrate-binding domain. The anal. of
binding
specificity of the chimeric lectin shows the presence of a
variable-binding region in legume lectins that determine their
carbohydrate-binding specificity. The result suggests the
presence of a
variable-binding region in legume lectins that determine their
carbohydrate-binding specificity.

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=> s (glycosyl hydrolase 74) or (gh74)
L6          10 (GLYCOSYL HYDROLASE 74) OR (GH74)

=> s l6 (6A) structure
L7           0 L6 (6A) STRUCTURE
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